

FIGURE 1 (SHEET 1)

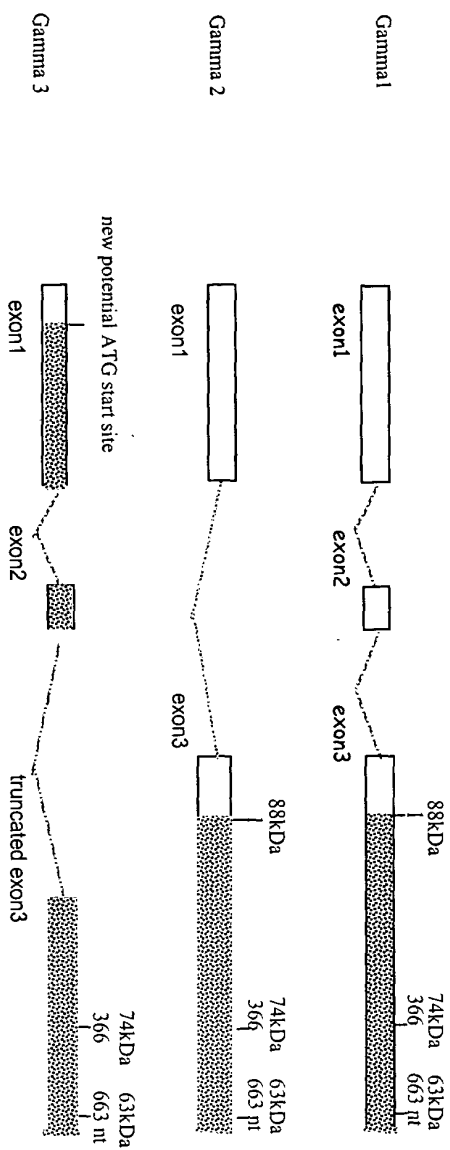
1 TGAAGCTCAGCTGATGCAGCCCGTTGGAGTGAGCTCATTTGCCGGGAACGAGCGAGTC 60  
 61 GCCCGTCAGCCCTAGTGAAGTGGCCCTGCATCCCGATTGTCTTCTCCCAAGGTCTAC 120  
 121 ATGATTACCTGAAGTTTAATAGTAAGACCATGAATTATGGCATTCTTAATGAAGCGT 180  
 181 TCAAGAAGTGAGAAGATGTCAAGAAAATAATGATTTTAAAGTATGTCTATTAACTCTG 240  
 241 ACTGTAGATATATATATTACCTCCTTAGTAATGCAAGAAGTGTGTTGGGAAGCAGAGA 300  
 T V D I Y I Y L L S N A R S V C G K Q R  
 301 AGCAAGCACTGTATTCTTGTCTCACCCTAAGCATTACTGGAGATAAGCCACATCAGT 360  
 S K Q L Y F L F S P K H Y W R I S H I S  
 361 CTACAAGAGGTTTTCATACAAACATAATAAGATGTAATGACCAAAAGTGAAGCACAT 420  
 L Q R G F H T N I I R C K W T K S E A H  
 421 TCTTGACGTAAGCACTGTACTCTCCAAGCAACCATGGTTTACATATTGGGATTTGAAA 480  
 S C S K H C Y S P S N H G L H I G I L K  
 481 CTTAGCACTTCTGCTCCCAAGGACTTACAAAGTGAACATTGTATGTCCCGTATTAA 540  
 L S T S A P K G L T K V N I C M S R I K  
 541 AGTACTTTGAACCTGTGTTCAAGGCTGTTTGGCAATCAAAATGAATGATTTCACGT 600  
 S T L N S V S K A V F G N Q N E M I S R  
 601 TTAGCTCAATTTAAGCCAGTCCCAATTTTAAAGAAAGTATCGGATAGTGGCTGTTA 660  
 L A Q F K P S S Q I L R K V S D S G W L  
 661 AAACAGAAAACATCAACACAGCCATCAATCTCTGA AAAAATATAGTGACAATCAGCA 720  
 K Q K N I K Q A I K S L K K Y S D K S A  
 721 GAAAAGAGTCTTTTCCAGAGAGAAAAGTCACTTATAGACAAAGAGAAGATATAGT 780  
 E K S P F P E E K S H I I D K E E D I G  
 781 AAACGAGTCTTTTTCATTACACAAAGTCTATAACCAAAATTTGGAGACTCATTTCTAC 840  
 K R S L F H Y T S S I T T K F G D S F Y  
 841 TTTTATCAATCATATTAATTATATTTCAAACGTAAAGAAAAATGTCTCAACAAAAAG 900  
 F L S N H I N S Y F K R K E K M S Q Q K  
 901 GAAAATGAACATTTCCGGGACAAATCAGAACTTGAAGATAAAAAGTAGAAGAGGGAAA 960  
 E N E H F R D K S E L E D K K V E E G K  
 961 TTAAGATCTCCAGATCCGTGGCATCTGGCTTATAAGCCAGGCTCAGAATCTGTACATACG 1020  
 L R S P D P G I L A Y K P G S E S V H T  
 1021 GTGACAAAGCCTACAAAGTCTTCTGCGATACTGATGTCTTCAAGTTTCAACTAAACAA 1080

V D K P T S P S A I P D V L Q V S T K Q  
1081 AGATTGCTAACTTTCTTCTCGTCCACGGAAGGTGTACAAGCTTTAGTAGGTGTTAT 1140  
S I A N F L S R P T E G V Q A L V G G Y  
1141 ATTGGTGCACTGTCCCAAAATTAAAGTATGATTCAAGAGTCAGTCAGAAGAACAGGAA 1200  
I G G L V P K L K Y D S K S Q S E E Q E  
1201 GAGCCTGTAAAACTGATCAGGCTGTACGCAAGACAGAAATGCAGAGGAGAAAAAGCGT 1260  
E P A K T D Q A V S K D R N A E E K K R  
1261 TTATCTCTTCAGCGAAGAAAGATTATCGCAAGGTTAGTATTGATAACAGGACCCGGGCA 1320  
L S L Q R E K I I A R V S I D N R T R A  
1321 TTAGTTCAGGCATTAAAGAAACAACACTGACCCAAAGCTCTGCATTACTAGGGTTGAAGAA 1380  
L V Q A L R R T T D P K L C I T R V E E  
1381 CTGACTTTTCATCTTCTAGAAATTTCTGAAGAAAAGAGTGGCTGTCAAGGAAAGAATT 1440  
L T F H L L E F P E G K G V A V K E R I  
1441 ATTCCATATTTATTACGACTGAGACAATTAAAGATGAACCTCTTCAGGCTGCAGTTAGA 1500  
I P Y L L R L R Q I K D E T L Q A A V R  
1501 GAAATTTGGCCCTAATTGGCTATGTGATCCAGTGGAAGGAGAGCAATCCGAATTCTC 1560  
E I L A L I G Y V D P V K G R G I R I L  
1561 TCAATTGATGGTGAGGAACAAGGGGCGTGTGCTCCAGACCCTACGAAAATTAGTT 1620  
S I D G G G T R G V V A L Q T L R K L V  
1621 GAACTTACTCAGAAGCCAGTTTCATCAGCTCTTTGATTACATTTGTGTGTTAAGCAGGT 1680  
E L T Q K P V H Q L F D Y I C G V S T G  
1681 GCCATATTAGCTTTCAATGTTGGGTTGTTTCATATGCCCCTTGGATGAATGTGAGGAAGCTT 1740  
A I L A F M L G L F H M P L D E C E E L  
1741 TATCGAAAATTAGGATCAGATGATTTTTCACAAAATGTCAATTGTTGGAACAGTAAAAATG 1800  
Y R K L G S D V F S Q N V I V G T V K M  
1801 AGTTGAGCCATGATCTTTATGACAGTCAAAACATGGGAAAAACATTTCTTAAGATAGGATG 1860  
S W S H A F Y D S Q T W E N I L K D R M  
1861 GGATCTGCACATGATGATTGAAACAGCAAGAAACCCACATGTCTTAAGTAGCTGCTGTA 1920  
G S A L M I E T A R N P T C P K V A A V  
1921 AGTACCATTAGTAATAGAGGATAACACCCAAAGCTTTTGTGTTCAGAAACTATGTGCAT 1980  
S T I V N R G I T P K A F V F R N Y G H  
1981 TTTCCTGGAATCAACTCTCATTTATTTGGGAGGCTGTCAGTATAAATGTGGCAGGCCATT 2040  
F P G I N S H Y L G G C Q Y K M W Q A I

2041	AGAGCCTCATCTGCTGCTCCAGGCTACTTTGCAGAAATATGCATTGGGAATGATCTTCAT	2100
	R A S S A A P G Y F A E Y A L G N D L H	
2101	CAAGATGGAGGTTTGCTTCTGAATTAACCTTCGGCATTAGCTATGCATGAGTGTAATGT	2160
	Q D G G L L L N N P S A L A M H E C K C	
2161	CTTTGGCCAGATGTGCCGTTAGAGTGCATAGTATCCCTGGGCACTGGACGTTATGAGAGT	2220
	L W P D V P L E C I V S L G T G R Y E S	
2221	GATGTGAAACACGCGTAACATACACAAGCTTGA AAAACTTAACTTTCTAATGTTATCAAC	2280
	D V R N T V T Y T S L K T K L S N V I N	
2281	AGTGCTACAGATACAGAAGAAGTCCATATAATGCTTGATGGCCTGTACCTCCTGACACC	2340
	S A T D T E E V H I M L D G L L P P D T	
2341	TATTTAGATTCAATCCTGTATATGTGAAACACATACCTCTAGATGAAGTCGAATGAA	2400
	Y F R F N P V M C E N I P L D E S R N E	
2401	AAGCTGCATCAGCTGCAGTTGGAAAGGTTGAATACATAGAAGAAATGAACAAAATG	2460
	K L D Q L Q L E G L K Y I E R N E Q K M	
2461	AAAAAAGTTGCAAAAATATTAAAGTCAGA AAAAAACAACCTCGCAGAAAATTAATGATTGG	2520
	K K V A K I L S Q E K T T L Q K I N D W	
2521	ATAAAATTAAAAA CTGATATGTATGAAGCACTTCCATTCTTTCAA AATTGTGATGAGTA	2580
	I K L K T D M Y E G L P F <u>S</u> <u>K</u> <u>L</u> -	
2581	TATGCTTATGTTCTCATAAATGAAGCTCTGTTAGAAAGTCAACCAACATTCAAATAAGGAA	2640
2641	TGTGGGGTTGCACATGAGTTAACTTTGAAATACGTATGAATTTCTGGAGAAATCCTGAAAA	2700
2701	AGACGGTGCTTCAACCAAGCTTGCATAGCACAGAGAATATTTCTGGTTACAGAATTCAATAT	2760
2761	GGGAAGCTAGGCTTTTAAAGATGTTAATAATTAGCTAAGCTTTAGTAACCCCTTACTGTGCTA	2820
2821	GTAGATTTTAGTAGATAATTGGTGTATATATGTTTGATGTTGAAATATATATAATATG	2880
2881	TGCCGAACAAGAAACCGAAAGCTATATTTGTA CTGTGATTTTAACTTTAGTCCCTCAATAAT	2940
2941	CATGTTGAATTTATGTGATCATTTGATTTTATTTTCATATGGAAGAAAGCTAATTTCTTTAA	3000
3001	ATTTACATTACCTAATAATTTCTCACTAGCTATGTTCTCCAATCCACACTGCCTTTTATGT	3060
3061	AATATCATCTAATAAGATGCAGAAAAATGGAATTTTCTCTAATTAAGTATTTTACAATTTG	3120
3121	ACATAAAAAAGAACCAAGATACAGTTTCTATTCAGATATGTTTATTTTAAACATTGTTGG	3180
3180	TTAAAAAAGGTGAAGTTCCAGTCAACCACTTTTACCCCTGAAATTTCAAGATAATGCTA	3240
3241	TATTAATCTTTCCAGATCTAACA CTAGCTTATTTCTTCCCTGTTAATAAATGGTTGAAC	3300
3301	TACTGAGGAGATATTCCTATCATTTAACAAAAATAAACTAATTTAATAATATCTGTTGTTAAA	3360
3361	AGGCTAATGTCA TTTTAAAAATTAA TTTTGTTCATATATGTAGCTCCCTTTAGCCTTTGA	3420

FIGURE 2

# iPLA2 $\gamma$ Splice Variants



open boxes are noncoding regions  
shaded regions are putative coding regions  
stippled lines represent intron splicing

4/5/00

80

M Q A G W S G R H C R E R A S R R C S P S D

160

CG LHPDCLLQGLHDDYLLKFFNN

140

220

N A R S V C G K Q R S K Q L Y F L

FIGURE 4 (SHEET 1)

## Full-length iPLA2 $\gamma$

### Primers for PCR amplification of full-length 88kDa iPLA2 $\gamma$ :

Sense primer M444 5'-TTTGTGACATGCTATTAATCTGACTGTAGATA-3'

Reverse primer M458 5'-GCATAGCATGCTCACAATTTGAAAAGAAATGGAAGTCC-3'

**Sequence of 88kDa iPLA2 gamma:**

atgtctattaactgtgactgttagatatatatattaccctccttagtaatgcagaagtgtt  
M S I N L T V D I Y I Y L L S N A R S V  
tgttggaagcagagaagcaagcaactgttattctgttctcaccataagcattactgyagg  
C G K Q R S K Q L Y F L F S P K H Y W R  
ataagccacatccagtctacaagaaggttttcatacaacaataaagatgtaaatgacc  
I S H I S L Q R G F H T N I I R C K W T  
aaaagtgaagcacattcttgcagtaagcactgttactctccaagcaaccatggtttacat  
K S E A H S C S K H C Y S P S N H G L H  
attggattttgaaacttagcacttctgtcccaaggygacttacaaaagtgaacattgt  
I G I L K L S T S A P K G L T K V N I C  
atgtcccgatattaagaagtacttgaactctgtttccaaggctgttttggcaatccaat  
M S R I K S T L N S V S K A V F G N Q N  
gaaatgatttcacglttagctcaatttaagccaagttcccaaattttaagaaaagtatcg  
E M I S R L A Q F K P S S Q I L R K V S  
gatagtgcgtglttaaacacagaaaacaacatcaaacagcgcataatctctgaaaaaatat  
D S G W L K Q K N I K Q A I K S L K K Y  
agtgcacaatcagcgagaaaagagtccttttcagaagagaaaagtcacattatagacaaa  
S D K S A E K S P F P E E K S H I I D K  
gaagaagatatagyttaaacygcagtcctttttcatcacacaagttctataaccacaaaattt  
E E D I G K R S L F H Y T S S I T T K F  
ggagactcatcttacttttatccaatcataattaattcatattccaacytaaggaaaaa  
G D S F Y F L S N H I N S Y F K R K E K  
atgtctcaacaaaagaaaatgaacatttcggygacaatatcagaacttgaagataaaaag  
M S Q Q K E N E H F R D K S E L E D K K

FIGURE 4 (SHEET 2)

gtagaagaggggaaattaagatctccagatccctgcatccctggttataagccaggctca  
V E E G K L R S P D P G I L A Y K P G S  
gaatctgtacatacgytggacaagcctacaagtccttctcgatataccctgatgttcttcaa  
E S V H T V D K P T S P S A I P D V L Q  
gttcaactaaacaagtalgtctaacttcttctcgtcccaaggaagtggtacaagct  
V S T K Q S I A N F L S R P T E G V Q A  
ttaagtggtgtatatgtgtgactgttcccccaatlaagtalgtatccaagagtcag  
L V G G Y I G G L V P K L K Y D S K S Q  
tcagaagaacaggaagcctgtctaaactgatcaggctgtcagcaagacagaatgca  
S E E Q E E P A K T D Q A V S K D R N A  
gaagagaaaaaagcgttatctcttcagcgagaaaaagattatcgcaaggytgatgtatgat  
E E K K R L S L Q R E K I I A R V S I D  
aacaggaccgggcattagttcaggcattagaagaacaactgacccaagctctgcatt  
N R T R A L V Q A L R R T T D P K L C I  
actaggytgaagaactgacttctcattctctagaatttctcgaaggaaagagtggt  
T R V E E L T F H L L E F P E G K G V A  
gtcaaggaagaattattccatatattattacgactgagacaatlaaggatgaactct  
V K E R I I P Y L L R L R Q I K D E T L  
caggctgcagttagagaatttggccctaattggtatgttgatccagtgaaagggaga  
Q A A V R E I L A L I G Y V D P V K G R  
ggaatccgaattctctcaattgatgtgtgaggaacaagggcggtgtctctccagacc  
G I R I L S I D G G T R G V V A L Q T  
ctacgaaatlagttgaacttactcagaagccagtlcatcagctcttggattacattgt  
L R K L V E L T Q K P V H Q L F D Y I C  
ggtgtaagcacaggtgcatatagcttctcatgttgggtgttccatatgccccttgat  
G V S T G A I L A F M L G L F H M P L D  
gaaatgtgaggaacttatacgaaaaatlaggatcagatgtatttccaaaaatgtccattgt  
E C E E L Y R K L G S D V F S Q N V I V  
ggaacagtaaaaatgagtgtaggccatgcatltaacacagtcacaacatgggaaaaacatt  
G T V K M S W S H A F Y D S Q T W E N I  
cttaagatatgagtgatctgcactgatgtatgaacacagaagaacccaacatgtcct  
L K D R M G S A L M I E T A R N P T C P  
aaggtagctgtgtaagtagtaccatagtaaatagaggataacccaagcttctgtcttc

FIGURE 4 (SHEET 3)

K V A A V S T I V N R G I T P K A F V F  
 agaactatgtcatttttcctggaatcaactcatttatttggaggctgtcagtaaa  
 R N Y G H F P G I N S H Y L G G C Q Y K  
 atgtgcaggccattagagcctcatctgtgtctccaggctacttgcagaatatgcaty  
 M W Q A I R A S S A A P 'G Y F A E Y A L  
 ggaatgatcttcatacagaatggaggttcttctgaataacccttcggcattagctatg  
 G N D L H Q D G G L L L N N P S A L A M  
 catgagtgtaatgtctttggccagatgtgccgttagagtgcatagtatccctgggcaat  
 H E C K C L W P D V P L E C I V S L G T  
 ggacgltatgagagtgatgtgagaaaacacggttaacatacacaagcttgaaaaactaaactt  
 G R Y E S D V R N T V T Y T S L K T K L  
 tctaattgtatacaacagtgctacagatacagaagaagtcacataataatgtgtgagccty  
 S N V I N S A T D T E E V H I M L D G L  
 ttacctcctgacacctattttagatltcaatcctctgtaatgtgtgaaacatacactctagat  
 L P P D T Y F R F N P V M C E N I P L D  
 gaaagtcgaaatgaaaagcttgatccagctgcagttggaagggttgaatatacatagaaga  
 E S R N E K L D Q L Q L E G L K Y I E R  
 aatgaacaaaaaatgaaaaagltgcaaaaatatlaagtcagaagaaaaaacactctgcag  
 N E Q K M K K V A K I L S Q E K T T L Q  
 aaatlaatgattgataaaatlaaaactgatatgtatgaaggacttccattcttltca  
 K I N D W I K L K T D M Y E G L P F F S  
 aaattgtga  
 K L -



[illegible]

gagagagaaaaagcgcttatctctcttcagcgagaaaaagattatcgcaaggtgagtattgat  
E E K K R R L S L Q R E K I I A R V S I D  
aacagagaccgggcattagttcagggcattaaagaagaacaactgaccccaagctctgcatt  
N R T R A L V Q A L R R T T D P K L C I  
actaaggttgtaagaactgacttcttcacbtctctagaatttcctgaagaaagagtggt  
T R V E E L T F H L L E F P E G K G V A  
gtcaaggaagaattatccacataattattacgactgagacaattaaagtatgaactctt  
V K E R I I P Y L L R L R Q I K D E T L  
caggtctgagttagagaattttggccctaattggtctatgttgatccagtgaaaggagag  
Q A A V R E I L A L I G Y V D P V K G R  
ggaatccgaattctctcaattgtatgttgaggaacaaggcggtgtgtctctcagacc  
G I R I L S I D G G T R G V V A L Q T  
ctagaaaattagttgaacttactcagaagccagttcatcagctctttgattacattgt  
L R K L V E L T Q K P V H Q L F D Y I C  
ggtgtgaagcacaggtgcccattatagcttctcatgttggtgttttcatatcccttgat  
G V S T G A I L A F M L G L F H M P L D  
gaatgtgaggaactttatcgaaaaattagagatcagatgttatttcacaaaatgtcatgtt  
E C E E L Y R K L G S D V F S Q N V I V  
ggaacagtaaaaaatgagttggaggccatgcatlittatgacagtcacaaacatggyaaaaacatt  
G T V K M S W S H A F Y D S Q T W E N I  
cttaagatatgagtgatgctgctgactgtatgtatgtaaacagcaagaacccccacatgtcct  
L K D R M G S A L M I E T A R N P T C P  
aaggtagctgtgtgaagtacatagtaaatagagggatabaacaccaagcttltgtgttc  
K V A A V S T I V N R G I T P K A F V F  
agaactatgttcatttctcctggaatcaactctcatlatttgggaggtgtcagtataaa  
R N Y G H F P G I N S H Y L G G C Q Y K  
atgtgacagccatttagagcctcatctgctgctccaggtacttgcagatatgcatgtg  
M W Q A I R A S S A A P G Y F A E Y A L  
ggaatgatcttcatacaagatgaggttctgtctgataaaccttcgcattagctatg  
G N D L H Q D G G L L L N N P S A L A M  
catgagtgtaaatgtcttcttgccagatgtgcgcttagagtgcatagttatccctgggcatt  
H E C K C L W P D V P L E C I V S L G T  
ggacgttatgagagtgatgttgagaacacacggttaacatcacacaagcttgaacactaacctt

**FIGURE 5 (SHEET 3)**

FIGURE 6 (SHEET 1)

Sequence of 74kDa iPLA2 gamma:  
starting at amino acid 122 (nucleotide 364)

Primers for PCR amplification of 74kDa iPLA2γ:

Sense primer m533                      5'-TCAAGTCGACATGATTTCACGTTAGC-3'  
Reverse primer M458                    5'-GCATAGCATGCTCACAAATTTGAAAGAATGGAAGTCC-3'

atgatttcacggttagctcaatttaagccaagttcccaattttaagaaaagtatcg  
M I S R L A Q F K P S S Q I L R K V S  
gatatggtgctgttaaaaccagaaaaacatcaaaccaagccatcaatctctgaaaaatat  
D S G W L K Q K N I K Q A I K S L K K Y  
agtgaacaatcagcagaaaaagagtcctttccagaaagagaaaagtcacattatagacaaa  
S D K S A E K S P F P E E K S H I I D K  
gaagaagatataggtaaacgcagtccttttccattacacaaagttctataaccacaaaattt  
E E D I G K R S L F H Y T S S I T T K F  
ggagactcattctacttttlatcaaatcatattatcatttcaaacgtaaggaaaaa  
G D S F Y F L S N H I N S Y F K R K E K  
atgtctcaacaagaagaatgaacattccgggacaatcagaacttgaagataaaaaag  
M S Q Q K E N E H F R D K S E L E D K K  
gtagaagagggaatataagatctccagatccctgcatccctgcttataagccaggtca  
V E E G K L R S P D P G I L A Y K P G S  
gaatctgtacatacgttgacaagccctacaagtccttctgcgatacctgatgttcttcaa  
E S V H T V D K P T S P S A I P D V L Q  
gtttcaactaacaagtatgtctaactttcttctcgtccacggaagtgtaacaagct  
V S T K Q S I A N F L S R P T E G V Q A  
ttagtagtggttatattgtgtgactgtgcccaaatlaagtatgatccaagagtcag  
L V G G Y I G G L V P K L K Y D S K S Q  
tcagaagaacaggaagagcctgtctaaactgatcaggctgtcagcaagacagaatgca  
S E E Q E E P A K T D Q A V S K D R N A  
gaggaagaaaaagcgtttatctcttcagcgagaaaaagattatcgcaagggtgagttatgat  
E E K K R L S L Q R E K I I A R V S I D

FIGURE 6 (SHEET 2)

aacaggaccgggcattagttcaggcattaaagaacaactgacccaagctctgcatt  
N R T R A L V Q A L R R T T D P K L C I  
actagggttgaagaactgacttttcattcttctagaatttcctgaagaaaggagtggct  
T R V E E L T F H L L E F P E G K G V A  
gtcaaggaagaattattccattatttaccagctgagacaattaagatgaactcct  
V K E R I I P Y L L R L R Q I K D E T L  
caggctgcagttagagaattttggccctaattggtatgtggtaccagtgaaggaga  
Q A A V R E I L A L I G Y V D P V K G R  
ggaatccgaattcttccaattgatgtgtggaaggaacaaggggcgtgtgtctctccagacc  
G I R I L S I D G G T R G V V A L Q T  
ctacgaaaattagttgaacttactcagaagccagttcaccagctcttattacattgt  
L R K L V E L T Q K P V H Q L F D Y I C  
ggtgtaagcacagtgccatatagcttccattggtgtgtgttccatatgcccctggat  
G V S T G A I L A F M L G L F H M P L D  
gattgtgaggaaacttatacgaaaattagatcagatgtatttccaaaatgtcattgt  
E C E E L Y R K L G S D V F S Q N V I V  
ggaacagtaaaaatgagttggagccatgcatlittatgacagtcacaacatggygaaacatt  
G T V K M S W S H A F Y D S Q T W E N I  
cttaaggatagatggtctgcactgatgttgaaacagcaagaacccccacatgtcct  
L K D R M G S A L M I E T A R N P T C P  
aagtagctgtgtagtaagcatagtaaatagaggatatacaccacaagcttltgttc  
K V A A V S T I V N R G I T P K A F V F  
agaactatgtcatttctcctggaatcaactctcattatttggaggctgtcagltataa  
R N Y G H F P G I N S H Y L G G C Q Y K  
atgtggcagggcattagagcctcatctgtctgccaggtacttgcagaatatgcatly  
M W Q A I R A S S A A P G Y F A E Y A L  
ggaatgatcttcatcaagatgaggttcttctgaataacccttcggcattagctatg  
G N D L H Q D G G L L L N N P S A L A M  
catgagtgtaaatgtcttggccagatgtgcccgttagagtgcattatccctgggcact  
H E C K C L W P D V P L E C I V S L G T  
ggacgttatgagagtgtgtgagaacaacggttaacatacacaagcttgaaaactaaact  
G R Y E S D V R N T V T Y T S L K T K L  
tctaattgttatacacagtgctacagatatacagaagaagtcataataatgttgatggcctg

S N V I N S A T D T E E V H I M L D G L  
 ttacctctgcacacctattttagattcaatccctgtgaatgtgtgaaaaacacatacccttagat  
 L P P D T Y F R F N P V M C E N I P L D  
 gaaagtcgaaatgtaaaagctggtcagctgcagttggaagggttgaatatcatagaaaga  
 E S R N E K L D Q L Q L E G L K Y I E R  
 aatgaacaaaaaatgtaaaagttgcacaaaatatgaagtcagaaaaaaacacactgcag  
 N E Q K M K K V A K I L S Q E K T T L Q  
 aaaattaatgatgtgataaaatlaaaaactgatatgtatgaaggacttccattctttca  
 K I N D W I K L K T D M Y E G L P F F S  
 aaattgtga  
 K L -

Figure 1. The effect of the number of iterations on the accuracy of the proposed algorithm. The accuracy is measured by the percentage of correct classification. The number of iterations is 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, 210, 220, 230, 240, 250, 260, 270, 280, 290, 300, 310, 320, 330, 340, 350, 360, 370, 380, 390, 400, 410, 420, 430, 440, 450, 460, 470, 480, 490, 500, 510, 520, 530, 540, 550, 560, 570, 580, 590, 600, 610, 620, 630, 640, 650, 660, 670, 680, 690, 700, 710, 720, 730, 740, 750, 760, 770, 780, 790, 800, 810, 820, 830, 840, 850, 860, 870, 880, 890, 900, 910, 920, 930, 940, 950, 960, 970, 980, 990, 1000. The accuracy is 0.8, 0.85, 0.9, 0.95, 1.0.

FIGURE 7 (SHEET 1)

Sequence of 63kDa iPLA2 gamma  
starting at amino acid 221 (nucleotide 661)

Sense primer M530

5'-GTAAGTCGACATGTCTCAACAAAGG-3'

Reverse primer M458

5'GCATAGCATGCTCACAATTTGAAAGAATGGAAGTCC-3')

atgtctcaacaaaggaaatgaacatttccgggacaatcagaacttgaagataaaaag  
M S Q Q K E N E H F R D K S E L E D K K  
gtagaaggagggaattaatgaatctccagatccctggcatccctgtgtatataagccaggtca  
V E E G K L R S P D P G I L A Y K P G S  
gaatctgtacatacgttgacaagccatacaagtccttctcgataccctgatgttctcaa  
E S V H T V D K P T S P S A I P D V L Q  
gtttcaactaacaagaatgtatgttaacttcttctcgtccacggaaggtgtacaagct  
V S T K Q S I A N F L S R P T E G V Q A  
ttagtagtggttatatgtgtgactgtgtcccaatlaagtatgatccaagagtcag  
L V G G Y I G G L V P K L K Y D S K S Q  
tcagaagaacaggaagagcctgtctaaactgatcaggtgtcagcaagaagcagaatgca  
S E E Q E E P A K T D Q A V S K D R N A  
gaagagaataaagcgttatctcttcagcgagaataagattatcgcaagggtgagtatgat  
E E K K R L S L Q R E K I I A R V S I D  
aacagagcccggtcattagttcagcgatlaagaagaacactgacccaagctctgcatt  
N R T R A L V Q A L R R T T D P K L C I  
actaggttgaagaactgacttcttcatcttcttagaatttccctgaaggaaaggagtgct  
T R V E E L T F H L L E F P E G K G V A  
gtcaaggaaagaattatcccatatttatcagactgagacaatlaaggatgaactctt  
V K E R I I P Y L L R L R Q I K D E T L  
caggtcgagttagagaattttggccctaattggtctatgtggatccagtgaaagggaga  
Q A A V R E I L A L I G Y V D P V K G R  
ggaatccgaattctcgaattgatgtgtgagaacaagggtgtgtgtctctccagacc  
G I R I L S I D G G G T R G V V A L Q T  
ctacgaaaattagttgaacttactcagaagccagttcatcagctcttattacatttgt  
L R K L V E L T Q K P V H Q L F D Y I C

FIGURE 7 (SHEET 2)

ggtgtaagccacagtgccatatagcttccatgttggtgttccatatgcccctggat  
G V S T G A I L A F M L G L F H M P L D  
gaatgtgaagaaactttatcgaaaattagatcagatgtatttccacaaatgtcatgtt  
E C E E L Y R K L G S D V F S Q N V I V  
ggaacagtaaaaatgagtggaagcatgcatlittatgacagtcacaaacatggyaaaacat  
G T V K M S W S H A F Y D S Q T W E N I  
cttaagatagatggatctgcactgatgtgaacacagcaagaacaccccatgtcct  
L K D R M G S A L M I E T A R N P T C P  
aagtagctgtgtaagtaccatagtaaataggagataacacccaagcttltgttctc  
K V A A V S T I V N R G I T P K A F V F  
agaaactatgtcatttccctggaatcaactctcattatttgggagctgtcagtataa  
R N Y G H F P G I N S H Y L G G C Q Y K  
atgtggcagccattagagccctcatctgtctccagctacttgcagaatatgcatg  
M W Q A I R A S S A A P G Y F A E Y A L  
ggaatgatcttcataagaatggaggttcttctgaataacccttcggcattagctatg  
G N D L H Q D G G L L L N N P S A L A M  
catgagtgaatgtcttggccagatgtgcccgttagagtgcatagtatccctgggcact  
H E C K C L W P D V P L E C I V S L G T  
ggacgttatgagagtgatgtgagaacacacggtatacacaaagcttgaaaactaacct  
G R Y E S D V R N T V T Y T S L' K T K L  
tctaattatcaacagtgctacagatacagaagaagtcacataatgcttgatggcctg  
S N V I N S A T D T E E V H I M L D G L  
ttacctctgacacccattttagatccaatccctgtaatgttgtaaaaacatacctctagat  
L P P D T Y F R F N P V M C E N I P L D  
gaaagtcgaatgaaaagctgcatcagctgcagttggaaggttgaaatacatagaaga  
E S R N E K L D Q L Q L E G L K Y I E R  
aatgaacaaaaaatgaaaaaagtgcaaaaatatattagtcagaagaaaaaacactctgcag  
N E Q K M K K V A K I L S Q E K T T L Q  
aaaatlaatgattgataaaaatlaaaactgatattgtaaggaacttccattctttca  
K I N D W I K L K T D M Y E G L P F F S  
aaattgtga  
K L -



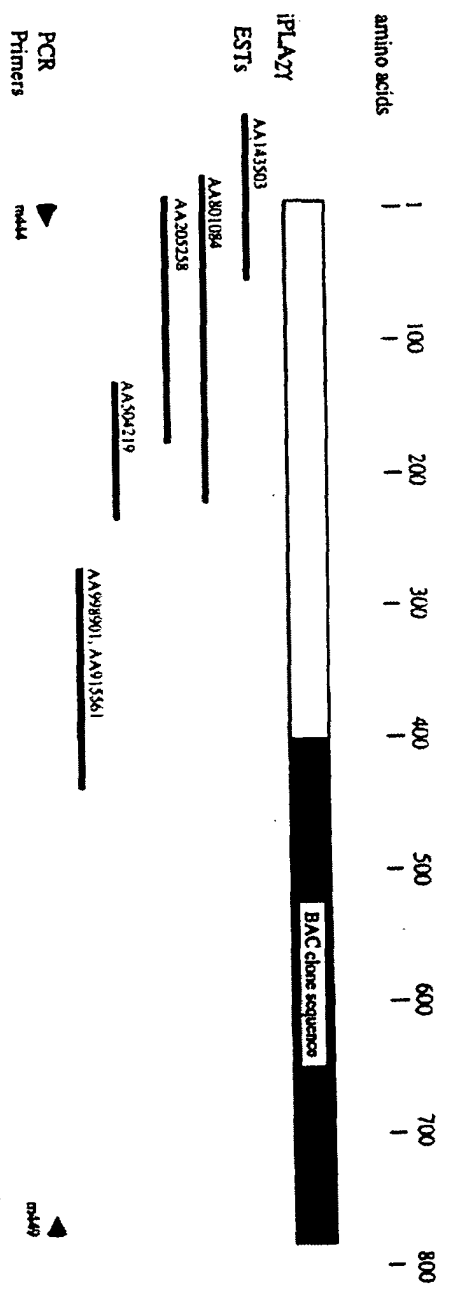


Fig. 8

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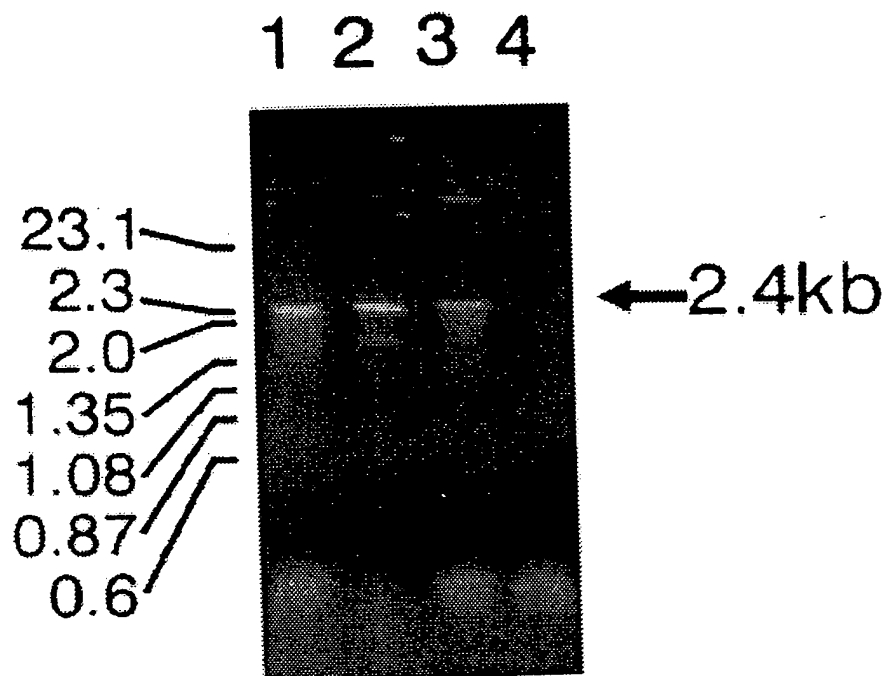


FIG. 9



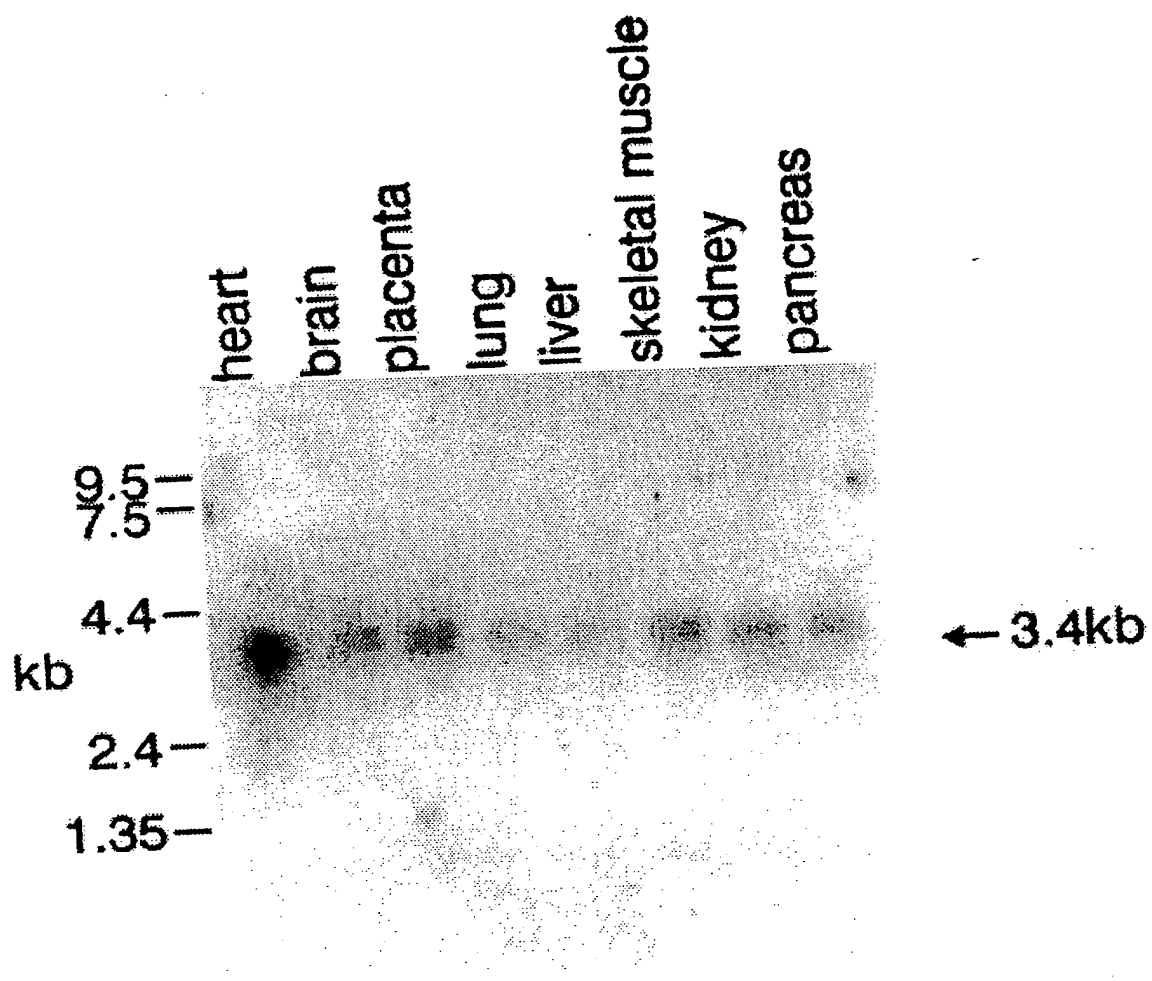
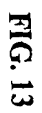


FIG. 12



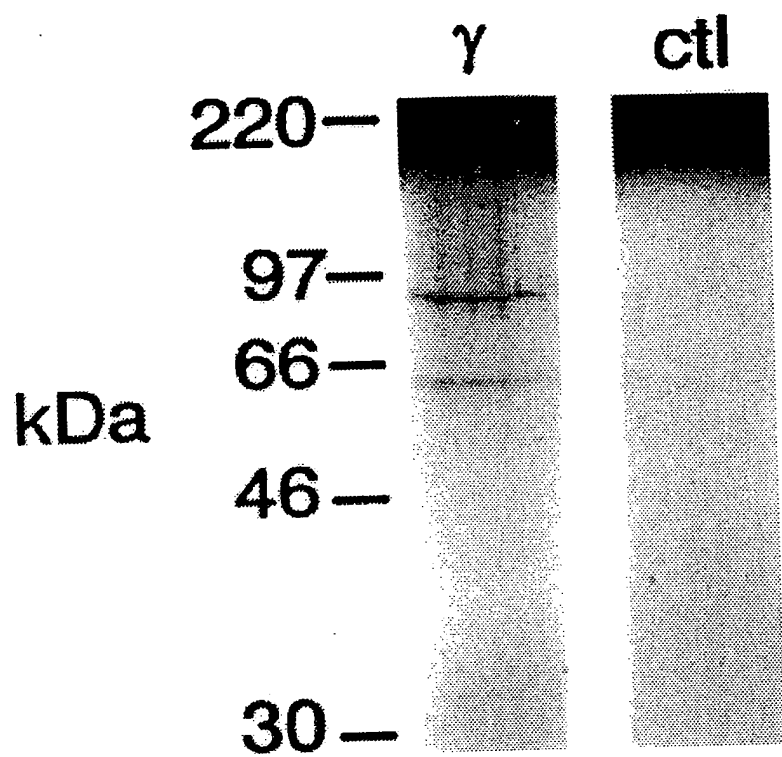


FIG. 14

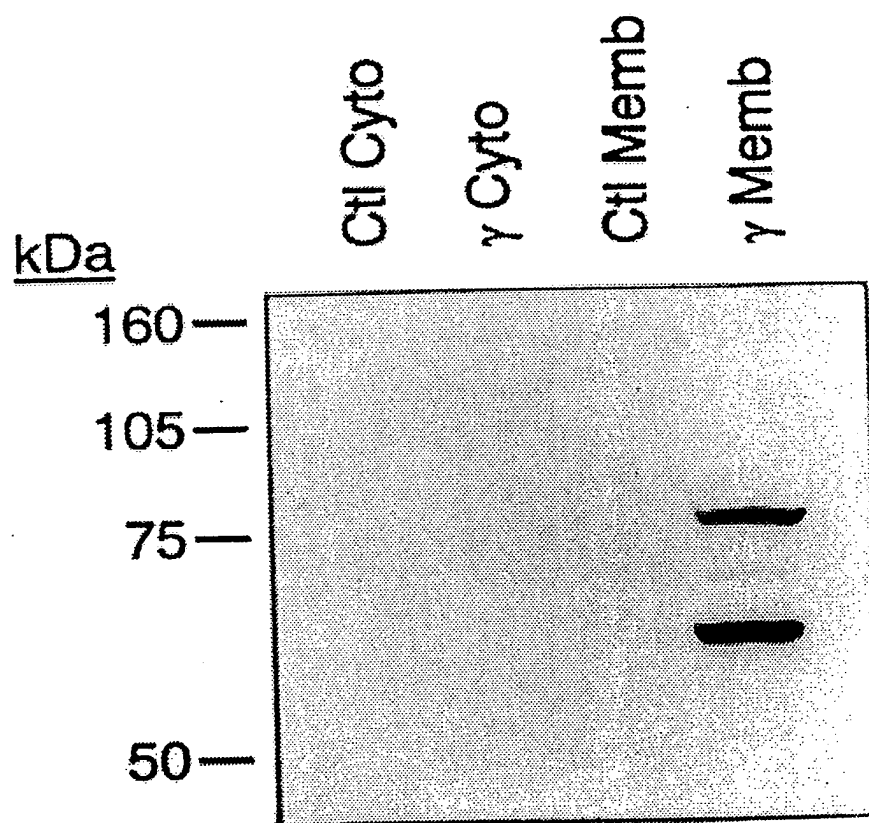


FIG. 15

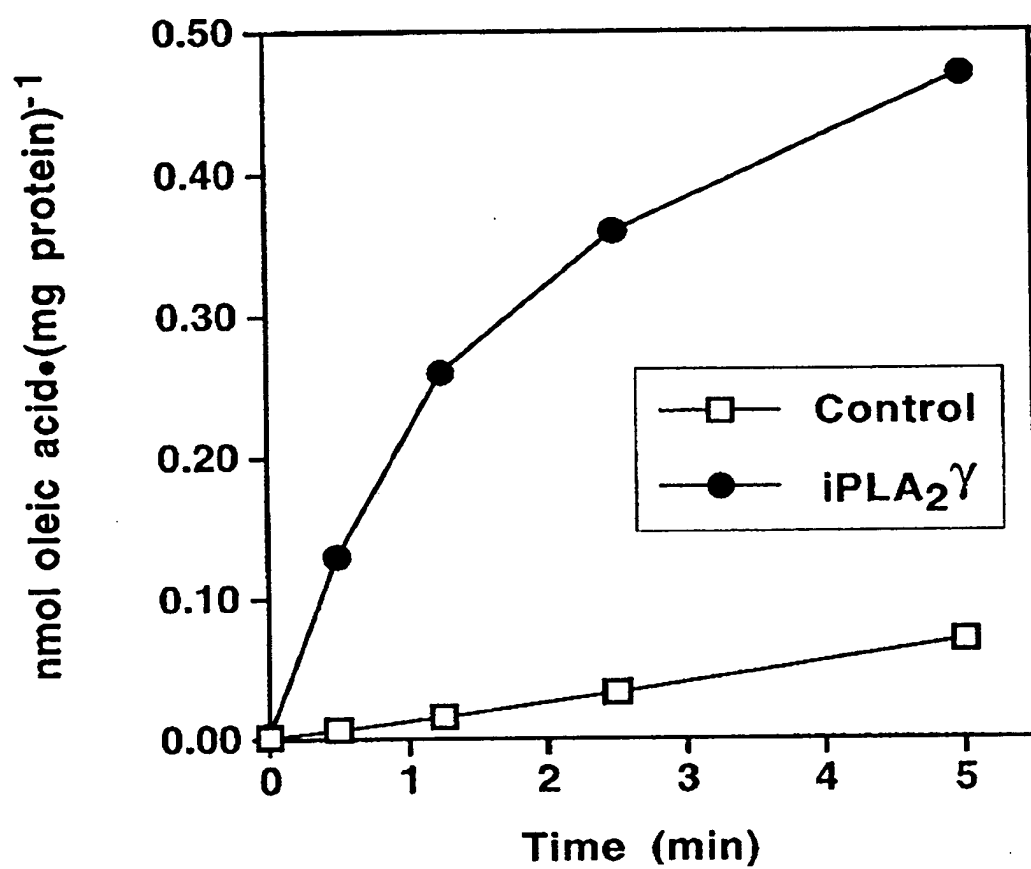


FIG. 16



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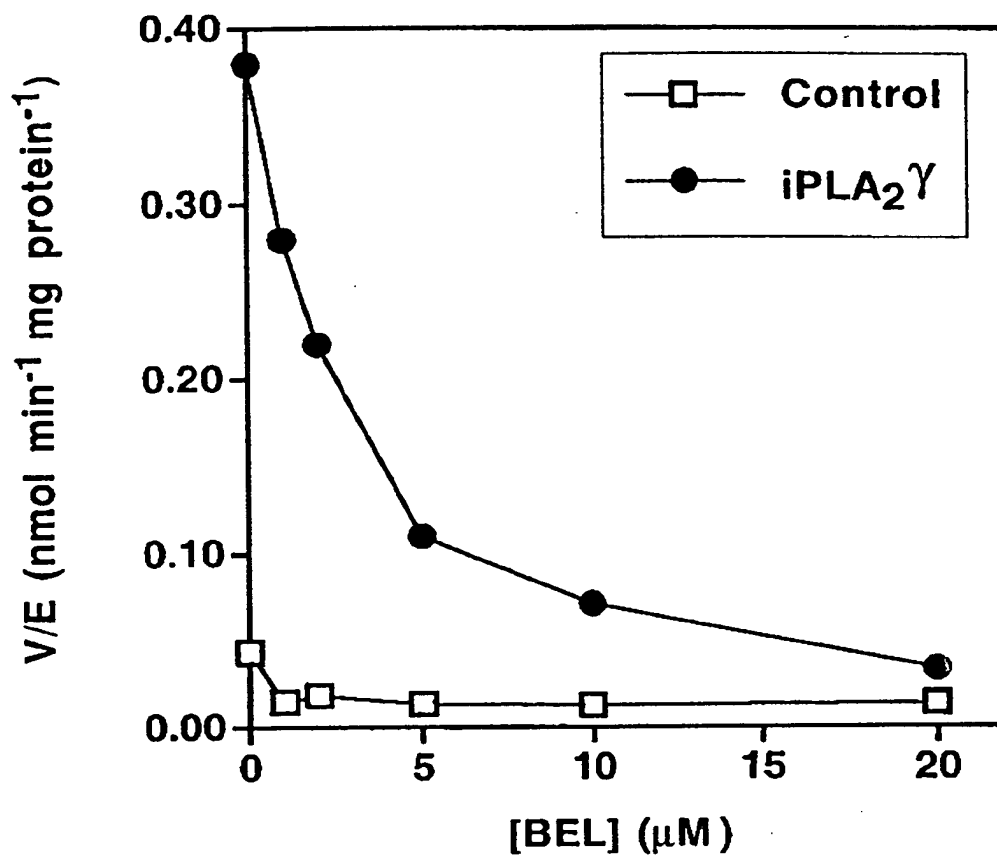


FIG. 18

# Translational Repression of iPLA<sub>2</sub>γ

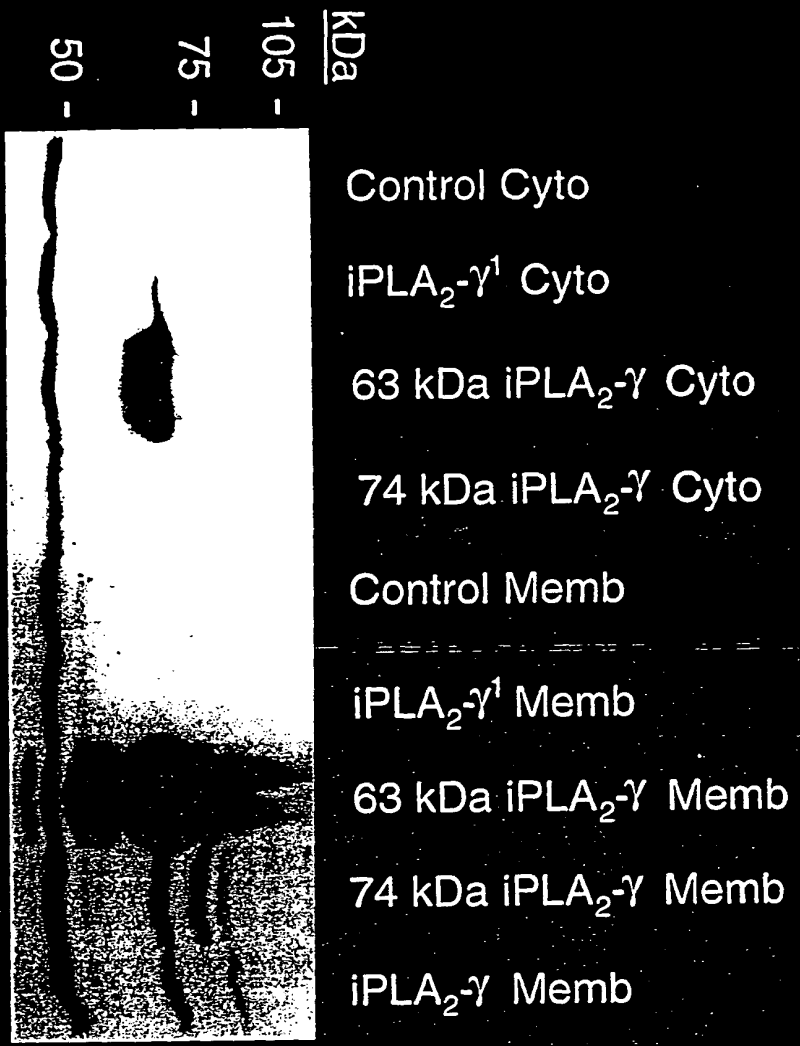


FIG. 19

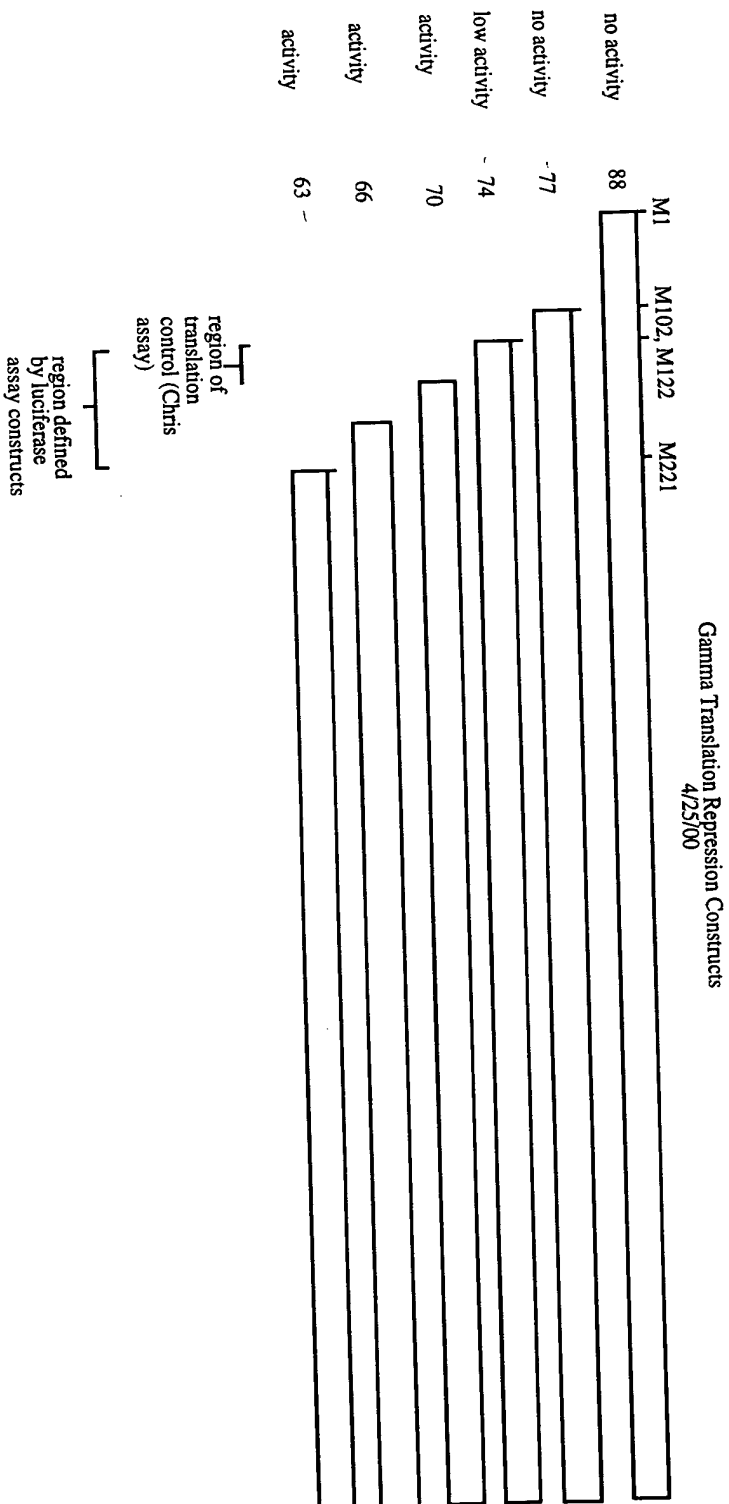


FIG. 20

FIG. 20 is a horizontal bar chart showing the results of a luciferase assay for various constructs. The y-axis lists the constructs: M1, M102, M122, and M221. The x-axis represents the activity level, with values 88, 77, 74, 70, 66, and 63. A bracket indicates the region of translation control (Chris assay) for constructs M102, M122, and M221. Another bracket indicates the region defined by luciferase assay constructs for all constructs.

Additionally, iPLA2y sequences were inserted by ligation of 15-23mer annealed phosphorylated oligonucleotide pairs 5' of full-length luciferase coding sequence cloned into pFASTBAC via NotI/XbaI restriction sites and then luciferase activity of recombinant protein produced in the Sf9 system was subsequently measured using the Luciferase Assay System of Promega.

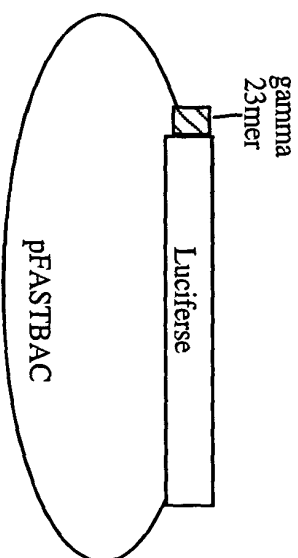


FIG. 21

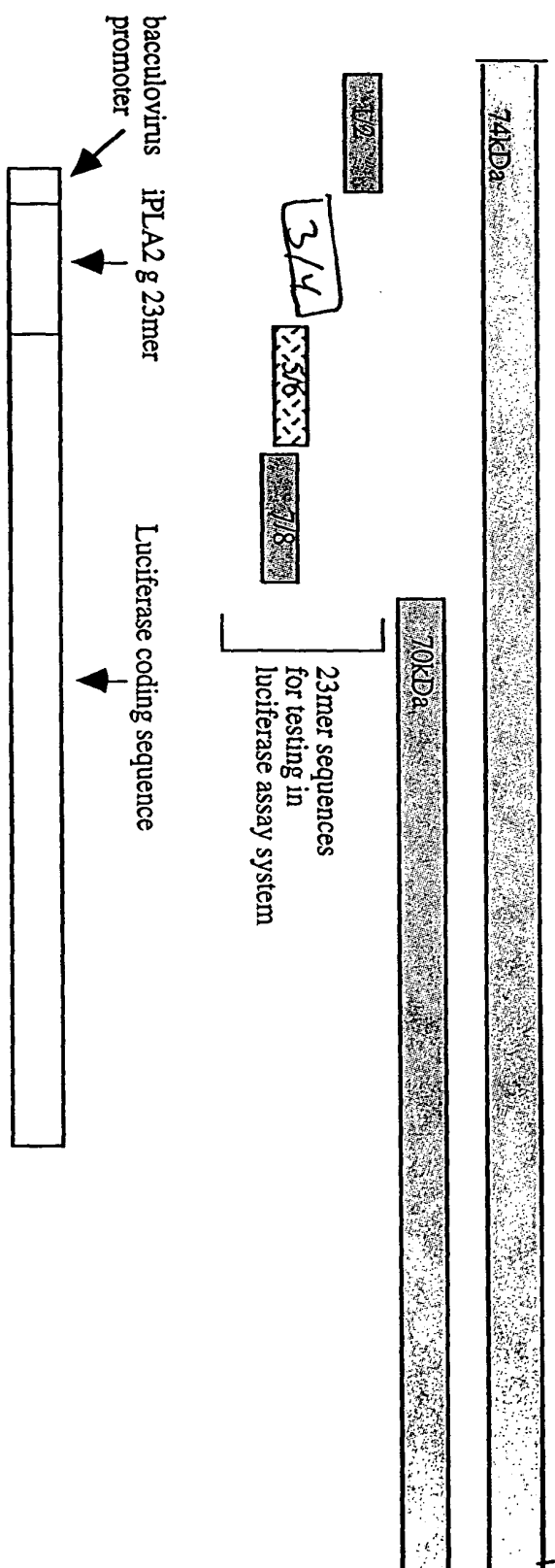


FIG. 22

Phosphorylated oligo pairs for sequence between nucleotide 364- 455  
for translational repression  
of iPLA2 gamma in the luciferase expression system:

iPLA2γ	atgattcacggttagctcaatttaagcccaagttcccaaatTTtaagaaagTatcgatagTgctggtTtaaaacagaaacatccaaca
1/2	tcgacctgatttcacggttagctcaatt ggactaaagTgcAaatcgagTtaaccg
3/4	tcgactaagcccaagTtcccaattTtaa gattcggttccaaggtTtaaatTtcg
5/6	tcgacgaaaagTatcgatagTgctg gctttcatagcctatcaccgaccccg
7/8	tcgacttaaaacagaaacatccaaca gaatttTgtcTttTgtagTtTgtccg

FIG. 23

Phosphorylated oligo pairs for sequence between nucleotide 364- 455  
for translational repression  
of iPLA2 gamma in the luciferase expression system:

Fig. 23

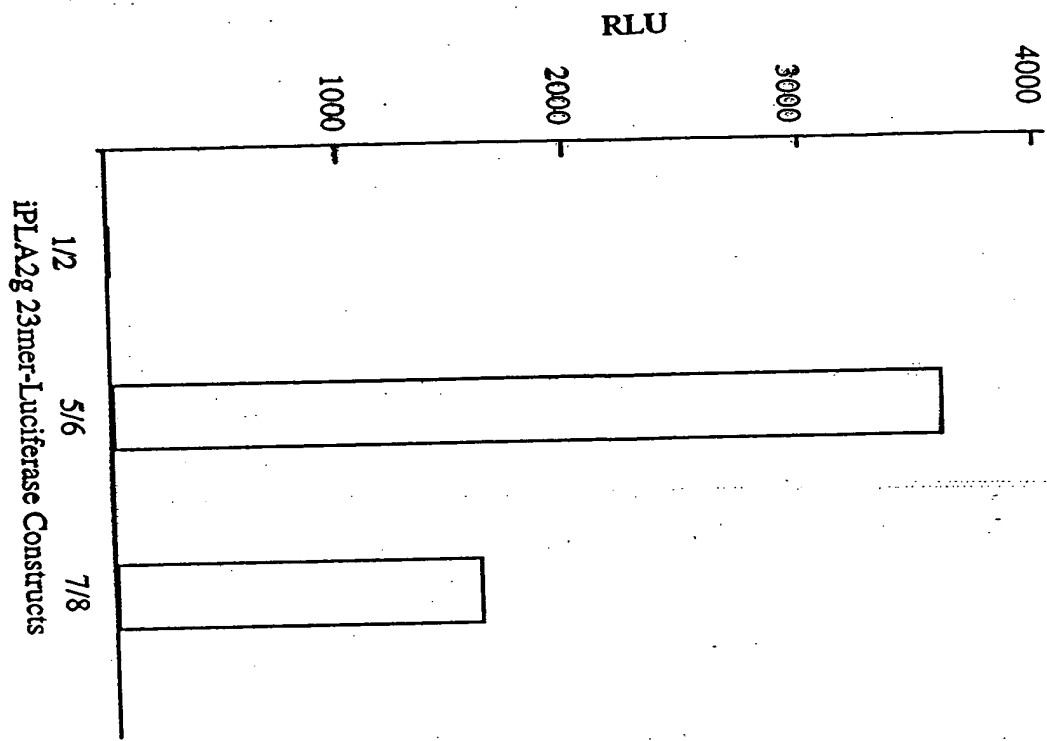


FIG. 24

FIG. 24 is a bar graph showing the relative luciferase activity (RLU) for three different iPLA2g 23mer-Luciferase Constructs. The y-axis is labeled 'RLU' and ranges from 0 to 4000. The x-axis is labeled 'iPLA2g 23mer-Luciferase Constructs' and has three categories: 1/2, 5/6, and 7/8. The bars are light gray with black outlines. The 1/2 construct shows the highest activity, followed by the 5/6 construct, and then the 7/8 construct.